

epo-FC-CIP-Jan2004.ST25
SEQUENCE LISTING

<110> Sun, Lee-Hwei K

Sun, Bill N

Sun, Cecily R

<120> Fc fusion proteins of human erythropoietin with high biological activities

<130> 02SUN2001-A

<140> to-be-assigned

<141> 2004-01-21

<150> 09/932812

<151> 2001-08-17

<160> 28

<170> PatentIn version 3.1

<210> 1

<211> 29

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<213> Artificial Sequence

<220>

<223> PCR primer

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<220>

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<213> Artificial Sequence

<220>

<223> PCR primer

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28

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tggtttctc gatggaggct gggaggcct 29

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aggcctccca gcctccatcg agaaaacca 29

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tttgtcga 69

<210> 8

<211> 21

<212> DNA

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<223> PCR primer

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gagtc当地at atggcccccc a 21

<210> 9

<211> 28

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<400> 9
ggaattctca tttacccaga gacaggga

28

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21

<210> 11

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60

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tggtccccca 70

<210> 13

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<400> 13

gacaaaactc acacatgccc a 21

<210> 14

<211> 23

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<220>

<223> PCR primer

<400> 14

acctgaagtc gcggggggac cgt 23

<210> 15

<211> 55

<212> DNA

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<223> PCR primer

<400> 15

gacaaaactc acacatgccc accgtgccc gcacctgaag tcgcgggggg accgt 55

<210> 16

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<211> 70

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR primer

<400> 16

cggatccggt ggccgttccg gtggaggcgg aagcggcggt ggaggatcag acaaaactca 60
cacatgcccc 70

<210> 17

<211> 1332

<212> DNA

<213> Artificial Sequence

<220>

<223> HuEPO-L-vFc gamma2 (Figure 2A)

<400> 17

aagcttggcg cggagatggg ggtgcacgaa tgtcctgcct ggctgtggct tctcctgtcc 60
ctgctgtcgc tccctctggg cctcccagtc ctgggcggcc caccacgcct catctgtgac 120
agccgagtcc tggagaggtt cctcttggag gccaaggagg ccgagaatat cacgacgggc 180
tgtgctgaac actgcagctt gaatgagaat atcactgtcc cagacaccaa agttaatttc 240
tatgccttggaa agaggatgga ggtcgccag caggccgtag aagtctggca gggcctggcc 300
ctgctgtcgg aagctgtcct gcggggccag gccctgtgg tcaactcttc ccagccgtgg 360
gagccctgc agctgcattt ggataaagcc gtcagtggcc ttgcagccct caccactctg 420
cttcgggctc tgggagccca gaaggaagcc atctccctc cagatgcggc ctcagctgct 480
ccactccgaa caatcactgc tgacactttc cgcaaactct tccgagtcta ctccaatttc 540
ctccggggaa agctgaagct gtacacaggg gaggcctgca ggacagggga cggatccgg 600
ggccgttccg gtggaggcgg aagcggcggt ggaggatcag agcgcataat ttgtgtcgag 660
tgcccaccgt gcccagcacc acctgtggca ggaccgtcag tcttcctt ccccccaaaa 720
cccaaggaca ccctcatgat ctcccgacc cctgaggtca cgtgcgtggt ggtggacgtg 780
agccacgaag accccgaggt ccagttcaac tggtacgtgg acggcgtgga ggtgcataat 840
gccaagacaa agccacggga ggagcagtcc aacagcacgt tccgtgtggt cagcgtcc 900

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| | |
|---|------|
| accgttgtgc accaggactg gctgaacggc aaggagtaca agtgcaaggt ctccaacaaa | 960 |
| ggcctcccg cctccatcga gaaaaccatc tccaaaacca aaggcagcc ccgagaacca | 1020 |
| caggtgtaca ccctgcccc atcccgagg gagatgacca agaaccagg cagcctgacc | 1080 |
| tgcctggtca aaggcttcta cccagcgcac atcgccgtgg agtggagag caatggcag | 1140 |
| ccggagaaca actacaagac cacacccc atgctggact ccgacggctc cttttccctc | 1200 |
| tacagcaagc tcaccgtgga caagagcagg tggcagcagg ggaacgttt ctcatgctcc | 1260 |
| gtgatgcatg aggctctgca caaccactac acgcagaaga gcctccctc gtctccgggt | 1320 |
| aatgagaat tc | 1332 |

<210> 18

<211> 436

<212> PRT

<213> Artificial sequence

<220>

<223> HuEPO-L-vFc gamma2 with a 27-amino acid leader peptide (Figure 2 A)

<400> 18

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Val | His | Glu | Cys | Pro | Ala | Trp | Leu | Trp | Leu | Leu | Ser | Leu |
| 1 | | | | 5 | | | | | 10 | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Leu | Pro | Leu | Gly | Leu | Pro | Val | Leu | Gly | Ala | Pro | Pro | Arg | Leu |
| | | | | 20 | | | | 25 | | | | | 30 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Cys | Asp | Ser | Arg | Val | Leu | Glu | Arg | Tyr | Leu | Leu | Glu | Ala | Lys | Glu |
| | | | | | 35 | | 40 | | | | | 45 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Glu | Asn | Ile | Thr | Thr | Gly | Cys | Ala | Glu | His | Cys | Ser | Leu | Asn | Glu |
| | | | | | 50 | | 55 | | | 60 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ile | Thr | Val | Pro | Asp | Thr | Lys | Val | Asn | Phe | Tyr | Ala | Trp | Lys | Arg |
| | | | | | 65 | | 70 | | 75 | | | | 80 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Val | Gly | Gln | Gln | Ala | Val | Glu | Val | Trp | Gln | Gly | Leu | Ala | Leu |
| | | | | | | | | 85 | | | | | 95 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Glu | Ala | Val | Leu | Arg | Gly | Gln | Ala | Leu | Leu | Val | Asn | Ser | Ser |
| | | | | | 100 | | | 105 | | | | | 110 | | |

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Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
180 185 190

Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
195 200 205

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
210 215 220

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
225 230 235 240

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
245 250 255

His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
260 265 270

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
275 280 285

Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn
290 295 300

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Ser
305 310 315 320

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln
325 330 335

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
340 345 350

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
355 360 365

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Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
370 375 380

Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
385 390 395 400

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
405 410 415

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
420 425 430

Ser Pro Gly Lys
435

<210> 19

<211> 1335

<212> DNA

<213> Artificial Sequence

<220>

<223> HuEPO-L-vFc gamma4 (Figure 2B)

<400> 19
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ctgctgtcgc tccctctggg cctcccagtc ctgggcggcc caccacgcct catctgtgac 120
agccgagtcc tggagaggtt cctcttggag gccaggagg ccgagaatat cacgacgggc 180
tgtgctgaac actgcagctt gaatgagaat atcactgtcc cagacaccaa agttaatttc 240
tatgcctgga agaggatgga ggtcgggcag caggccgtag aagtctggca gggcctggcc 300
ctgctgtcgg aagctgtcct gcggggccag gccctgttgg tcaactcttc ccagccgtgg 360
gagccctgc agctgcatgt ggataaagcc gtcagtggcc ttcgcagcct caccactctg 420
cttcgggctc tgggagccca gaaggaagcc atctccctc cagatgcggc ctcagctgct 480
ccactccgaa caatcactgc tgacactttc cgcaaactct tccgagtcta ctccaatttc 540
ctccgggaa agctgaagct gtacacaggg gaggcctgca ggacaggggga cggatccgg 600
ggcgggttccg gtggaggcgg aagcggcggt ggaggatcag agtccaaata tggtccccca 660
tgcccaccat gcccagcacc tgagttcgcg gggggaccat cagtcttcct gttccccca 720
aaacccaagg acactctcat gatctcccg acccctgagg tcacgtgcgt ggtggtggac 780
gtgagccagg aagaccccgaa ggtccagttc aactggtagc tggatggcgt ggaggtgcat 840

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aatgccaaga caaagccgcg ggagggagcag ttcaacagca cgtaccgtgt ggtcagcgtc 900
ctcaccgtcc tgcaccagga ctggctgaac ggcaaggagt acaagtgcaa ggtctccaac 960
aaaggcctcc cgtcctccat cgagaaaacc atctccaaag ccaaaggcga gccccgagag 1020
ccacaggtgt acaccctgcc cccatcccag gaggagatga ccaagaacca ggtcagcctg 1080
acctgctgg tcaaaggcctt ctaccccagc gacatcgccg tggagtggga gagcaatggg 1140
cagccggaga acaactacaa gaccacgcct cccgtgctgg actccgacgg ctcccttctc 1200
ctctacagca ggctaaccgt ggacaagagc aggtggcagg agggaaatgt cttctcatgc 1260
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ggtaaatgag aattc 1335

<210> 20

<211> 437

<212> PRT

<213> Artificial Sequence

<220>

<223> HuEPO-L-vFc gamma4 with a 27-amino acid leader peptide (Figure 2B
)

<400> 20

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
20 25 30

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
35 40 45

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
50 55 60

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
65 70 75 80

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
85 90 95

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
180 185 190

Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
195 200 205

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe
210 215 220

Ala Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
225 230 235 240

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
245 250 255

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
260 265 270

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
275 280 285

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
290 295 300

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
305 310 315 320

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
325 330 335

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
340 345 350

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
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355 360 365

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
370 375 380

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
385 390 395 400

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
405 410 415

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
420 425 430

Leu Ser Leu Gly Lys
435

<210> 21

<211> 1329

<212> DNA

<213> Artificial Sequence

<220>

<223> HuEPO-L-vFc gamma1 (Figure 2C)

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agccgagtcc tggagaggtt cctcttggag gccaaggagg ccgagaatat cacgacgggc 180
tgtgctgaac actgcagctt gaatgagaat atcactgtcc cagacaccaa agttaatttc 240
tatgcctgga agaggatgga ggtcgggcag caggccgtag aagtctggca gggcctggcc 300
ctgctgtcgg aagctgtcct gcggggccag gccctgttgg tcaactcttc ccagccgtgg 360
gagccctgc agctgcatgt ggataaagcc gtcagtggcc ttcgcagcct caccactctg 420
cttcgggctc tgggagccca gaaggaagcc atctccctc cagatgcggc ctcagctgct 480
ccactccgaa caatcactgc tgacactttc cgcaaactct tccgagtcta ctccaatttc 540
ctccggggaa agctgaagct gtacacaggg gaggcctgca ggacagggga cggatccggt 600
ggcgggtccg gtggaggcgg aagcggcggt ggaggatcag acaaaactca cacatgccca 660
ccgtgcccag cacctgaagt cgcgggggaa ccgtcagtct tcctttccc cccaaaaccc 720
aaggacaccc tcatgatctc ccggacacct gaggtcacat gcgtggtggt ggacgtgagc 780

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| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| cacgaagacc | ctgaggtcaa | gttcaactgg | tacgtggacg | gcgtggaggt | gcataatgcc | 840 |
| aagacaaagc | cgcgggagga | gcagtacaac | agcacgtacc | gggtggtcag | cgtcctcacc | 900 |
| gtcctgcacc | aggactggct | aatggcaag | gagtacaagt | gcaaggtctc | caacaaagcc | 960 |
| ctcccagcct | ccatcgagaa | aaccatctcc | aaagccaaag | ggcagccccg | agaaccacag | 1020 |
| gtgtacaccc | tgccccatc | ccgggatgag | ctgaccaaga | accaggtcag | cctgacctgc | 1080 |
| ctggtcaaag | gcttctatcc | cagcgacatc | gccgtggagt | gggagagcaa | tggcagccg | 1140 |
| gagaacaact | acaagaccac | gcctccgtg | ctggactccg | acggctcctt | cttcctctac | 1200 |
| agcaagctca | ccgtggacaa | gagcaggtgg | cagcagggga | acgtcttctc | atgctccgtg | 1260 |
| atgcatgagg | ctctgcacaa | ccactacacg | cagaagagcc | tctccctgtc | tccggtaaa | 1320 |
| tgagaattc | | | | | | 1329 |

<210> 22

<211> 435

<212> PRT

<213> Artificial Sequence

<220>

<223> HuEPO-L-vFc gamma1 with a 27-amino acid leader peptide (Figure 2c)

<400> 22

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Val | His | Glu | Cys | Pro | Ala | Trp | Leu | Trp | Leu | Leu | Ser | Leu |
| 1 | | | | 5 | | | | | 10 | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Leu | Pro | Leu | Gly | Leu | Pro | Val | Leu | Gly | Ala | Pro | Pro | Arg | Leu |
| | | | | 20 | | | | 25 | | | | 30 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Cys | Asp | Ser | Arg | Val | Leu | Glu | Arg | Tyr | Leu | Leu | Glu | Ala | Lys | Glu |
| | | | | | 35 | | 40 | | | | 45 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Glu | Asn | Ile | Thr | Thr | Gly | Cys | Ala | Glu | His | Cys | Ser | Leu | Asn | Glu |
| | | | | | 50 | | 55 | | | 60 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ile | Thr | Val | Pro | Asp | Thr | Lys | Val | Asn | Phe | Tyr | Ala | Trp | Lys | Arg |
| | | | | | 65 | | 70 | | | 75 | | | 80 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Val | Gly | Gln | Gln | Ala | Val | Glu | Val | Trp | Gln | Gly | Leu | Ala | Leu |
| | | | | | 85 | | | 90 | | | | 95 | | | |

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Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
100 105 110

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
115 120 125

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
130 135 140

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
145 150 155 160

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
165 170 175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
180 185 190

Gly Ser Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
195 200 205

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Val Ala Gly
210 215 220

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
225 230 235 240

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His
245 250 255

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val
260 265 270

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
275 280 285

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
290 295 300

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Ser Ile
305 310 315 320

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
325 330 335

Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
340 345 350

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Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
355 360 365

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
370 375 380

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
385 390 395 400

Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
405 410 415

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
420 425 430

Pro Gly Lys
435

<210> 23

<211> 16

<212> PRT

<213> Artificial sequence, 16-amino acid peptide linker

<400> 23

Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

<210> 24

<211> 15

<212> PRT

<213> Human IgG1 hinge sequence

<400> 24

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

<210> 25

<211> 10

<212> PRT

<213> Truncated human IgG1 hinge sequence

<400> 25

Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10

<210> 26

<211> 232

<212> PRT

<213> Human IgG1 Fc with native hinge, CH2 and CH3 domains

<400> 26

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
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170

175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
 225 230

<210> 27

<211> 228

<212> PRT

<213> Human IgG2 Fc with native hinge, CH2 and CH3 domains

<400> 27

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
 1 5 10 15

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 20 25 30

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 35 40 45

His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu
 50 55 60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
 65 70 75 80

Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn
 85 90 95

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro
 100 105 110

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln
 115 120 125

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Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
130 135 140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145 150 155 160

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
165 170 175

Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
180 185 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
195 200 205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
210 215 220

Ser Pro Gly Lys
225

<210> 28

<211> 229

<212> PRT

<213> Human IgG4 Fc with native hinge, CH2 and CH3 domains

<400> 28

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

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Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
130 135 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys
225